

Year	1960	1961	1962	1963	1964	1965	1966	1967	1968	1969	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1960	1961	1962	1963	1964	1965	1966	1967	1968	1969	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

(i) APPLICANT: Godowski, Paul J.
Gurney, Austin L.

(iii) NUMBER OF SEQUENCES: 17

(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 1 DNA Way
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080

(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(A) NAME: Dreger, Ginger R.
(B) REGISTRATION NUMBER: 33,055
(C) REFERENCE/DOCKET NUMBER: P1130

(A) TELEPHONE: 650/225-3216
(B) TELEFAX: 650/952-9881

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2290 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

GGCTGAGGGG	AGGCCCGGAG	CCTTTCTGGG	GCCTGGGGGA	TCCTCTTGCA	50
CTGGTGGGTG	GAGAGAAGCG	CCTGCAGCCA	ACCAGGGTCA	GGCTGTGCTC	100
ACAGTTTCCT	CTGGCGGCAT	GTAAAGGCTC	CACAAAGGAG	TTGGGAGTTC	150
AAATGAGGCT	GCTGCGGACG	GCCTGAGGAT	GGACCCCAAG	CCCTGGACCT	200
GCCGAGCGTG	GCACTGAGGC	AGCGGCTGAC	GCTACTGTGA	GGGAAAGAAG	250
GTTGTGAGCA	GCCCCGAGG	ACCCCTGGCC	AGCCCTGGCC	CCAGCCTCTG	300

CCGGAGCCCT	CTGTGGAGGC	AGAGCCAGTG	GAGCCCAGTG	AGGCAGGGCT	350
GCTTGGCAGC	CACCGGCCCTG	CAACTCAGGA	ACCCCTCCAG	AGGCCATGGA	400
CAGGCTGCCC	CGCTGACGGC	CAGGGTGAAG	CATGTGAGGA	GCCGCCCCGG	450
AGCCAAGCAG	GAGGGAAGAG	GCTTTCATAG	ATTCTATTCA	CAAAGAATAA	500
CCACCATTTT	GCAAGGACCA	TGAGGCCACT	GTGCGTGACA	TGCTGGTGGC	550
TCGGACTGCT	GGCTGCCATG	GGAGCTGTTG	CAGGCCAGGA	GGACGGTTTT	600
GAGGGCAC'TG	AGGAGGGCTC	GCCAAGAGAG	TTCATTTACC	TAAACAGGTA	650
CAAGCGGGCG	GGCGAGTCCC	AGGACAAGTG	CACCTACACC	TTCATTGTGC	700
CCCAGCAGCG	GGTCACGGGT	GCCATCTGCG	TCAACTCCAA	GGAGCCTGAG	750
GTGCTTCTGG	AGAACCGAGT	GCATAAGCAG	GAGCTAGAGC	TGCTCAACAA	800
TGAGCTGCTC	AAGCAGAAGC	GGCAGATCGA	GACGCTGCAG	CAGCTGGTGG	850
AGGTGGACGG	CGGCATTGTG	AGCGAGGTGA	AGCTGCTGCG	CAAGGAGAGC	900
CGCAACATGA	ACTCGCGGGT	CACGCAGCTC	TACATGCAGC	TCCTGCACGA	950
GATCATCCGC	AAGCGGGACA	ACGCGTTGGA	GCTCTCCCAG	CTGGAGAACA	1000
GGATCCTGAA	CCAGACAGCC	GACATGCTGC	AGCTGGCCAG	CAAGTACAAG	1050
GACCTGGAGC	ACAAGTACCA	GCACCTGGCC	ACACTGGCCC	ACAACCAATC	1100
AGAGATCATC	GCGCAGCTTG	AGGAGCACTG	CCAGAGGGTG	CCCTCGGCCA	1150
GGCCCGTCCC	CCAGCCACCC	CCCCTGCCC	CGCCCCGGGT	CTACCAACCA	1200
CCCACCTACA	ACCGCATCAT	CAACCAGATC	TCTACCAACG	AGATCCAGAG	1250
TGACCAGAAC	CTGAAGGTGC	TGCCACCCCC	TCTGCCCACT	ATGCCCACTC	1300
TCACCAGCCT	CCCATCTTCC	ACCGACAAGC	CGTCGGGCCC	ATGGAGAGAC	1350
TGCCTGCAGG	CCCTGGAGGA	TGGCCACGAC	ACCAGCTCCA	TCTACCTGGT	1400
GAAGCCGGAG	AACACCAACC	GCCTCATGCA	GGTGTGGTGC	GACCAGAGAC	1450
ACGACCCCGG	GGGCTGGACC	GTCATCCAGA	GACGCC'TGGA	TGGCTCTGTT	1500
AACTTCTTCA	GGAACTGGGA	GACGTACAAG	CAAGGGT'TTG	GGAACATTGA	1550
CGGCGAATAC	TGGCTGGGCC	TGGAGAACAT	TTACTGGCTG	ACGAACCAAG	1600
GCAACTACAA	ACTCCTGGTG	ACCATGGAGG	ACTGGTCCGG	CCGCAAAGTC	1650
TTTGCAGAAT	ACGCCAGTTT	CCGCC'TGGAA	CCTGAGAGCG	AGTATTATAA	1700
GCTGCGGCTG	GGGCGCTACC	ATGGCAATGC	GGGTGACTCC	TTTACATGGC	1750
ACAACGGCAA	GCAGTTCACC	ACCCTGGACA	GAGATCATGA	TGTCTACACA	1800
GGAAACTGTG	CCCACTACCA	GAAGGGAGGC	TGGTGGTATA	ACGCC'TGTGC	1850

CCACTCCAAC	CTCAACGGGG	TCTGGTACCG	CGGGGGCCAT	TACCGGAGCC	1900
GCTACCAGGA	CGGAGTCTAC	TGGGCTGAGT	TCCGAGGAGG	CTCTTACTCA	1950
CTCAAGAAAG	TGGTGATGAT	GATCCGACCG	AACCCCAACA	CCTTCCACTA	2000
AGCCAGCTCC	CCCTCCTGAC	CTCTCGTGGC	CATTGCCAGG	AGCCCACCCCT	2050
GGTCACGCTG	GCCACAGCAC	AAAGAACAAC	TCCTCACCAG	TTCATCCTGA	2100
GGCTGGGAGG	ACCGGGATGC	TGGATTCTGT	TTTCCGAAGT	CACTGCAGCG	2150
GATGATGGAA	CTGAATCGAT	ACGGTGTTTT	CTGTCCCTCC	TACTTTCCTT	2200
CACACCAGAC	AGCCCCTCAT	GTCTCCAGGA	CAGGACAGGA	CTACAGACAA	2250
CTCTTTCTTT	AAATAAATTA	AGTCTCTACA	ATAAAAAAAAA		2290

(2) INFORMATION FOR SEQ ID NO:2:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

				170					175					180
His	Lys	Tyr	Gln	His 185	Leu	Ala	Thr	Leu	Ala 190	His	Asn	Gln	Ser	Glu 195
Ile	Ile	Ala	Gln	Leu 200	Glu	Glu	His	Cys	Gln 205	Arg	Val	Pro	Ser	Ala 210
Arg	Pro	Val	Pro	Gln 215	Pro	Pro	Pro	Ala	Ala 220	Pro	Pro	Arg	Val	Tyr 225
Gln	Pro	Pro	Thr	Tyr 230	Asn	Arg	Ile	Ile	Asn 235	Gln	Ile	Ser	Thr	Asn 240
Glu	Ile	Gln	Ser	Asp 245	Gln	Asn	Leu	Lys	Val 250	Leu	Pro	Pro	Pro	Leu 255
Pro	Thr	Met	Pro	Thr 260	Leu	Thr	Ser	Leu	Pro 265	Ser	Ser	Thr	Asp	Lys 270
Pro	Ser	Gly	Pro	Trp 275	Arg	Asp	Cys	Leu	Gln 280	Ala	Leu	Glu	Asp	Gly 285
His	Asp	Thr	Ser	Ser 290	Ile	Tyr	Leu	Val	Lys 295	Pro	Glu	Asn	Thr	Asn 300
Arg	Leu	Met	Gln	Val 305	Trp	Cys	Asp	Gln	Arg 310	His	Asp	Pro	Gly	Gly 315
Trp	Thr	Val	Ile	Gln 320	Arg	Arg	Leu	Asp	Gly 325	Ser	Val	Asn	Phe	Phe 330
Arg	Asn	Trp	Glu	Thr 335	Tyr	Lys	Gln	Gly	Phe 340	Gly	Asn	Ile	Asp	Gly 345
Glu	Tyr	Trp	Leu	Gly 350	Leu	Glu	Asn	Ile	Tyr 355	Trp	Leu	Thr	Asn	Gln 360
Gly	Asn	Tyr	Lys	Leu 365	Leu	Val	Thr	Met	Glu 370	Asp	Trp	Ser	Gly	Arg 375
Lys	Val	Phe	Ala	Glu 380	Tyr	Ala	Ser	Phe	Arg 385	Leu	Glu	Pro	Glu	Ser 390
Glu	Tyr	Tyr	Lys	Leu 395	Arg	Leu	Gly	Arg	Tyr 400	His	Gly	Asn	Ala	Gly 405
Asp	Ser	Phe	Thr	Trp 410	His	Asn	Gly	Lys	Gln 415	Phe	Thr	Thr	Leu	Asp 420
Arg	Asp	His	Asp	Val 425	Tyr	Thr	Gly	Asn	Cys 430	Ala	His	Tyr	Gln	Lys 435
Gly	Gly	Trp	Trp	Tyr 440	Asn	Ala	Cys	Ala	His 445	Ser	Asn	Leu	Asn	Gly 450
Val	Trp	Tyr	Arg	Gly 455	Gly	His	Tyr	Arg	Ser 460	Arg	Tyr	Gln	Asp	Gly 465
Val	Tyr	Trp	Ala	Glu 470	Phe	Arg	Gly	Gly	Ser 475	Tyr	Ser	Leu	Lys	Lys 480

ACCACCTGAT	CTGGCAACTT	CTCCCACCAA	AAGCCCTTTC	AAGATACCAC	1250
CGGTAAC TTT	CATCAATGAA	GGACCATTCA	AAGACTGTCA	GCAAGCAAAA	1300
GAAGCTGGGC	ATTTCGGTCAG	TGGGATTTTAT	ATGATTAAAC	CTGAAAACAG	1350
CAATGGACCA	ATGCAGTTAT	GGTGTGAAAA	CAGTTTGGAC	CCTGGGGGTT	1400
GGACTGTTAT	TCAGAAAAGA	ACAGACGGCT	CTGTCAACTT	CTTCAGAAAT	1450
TGGGAAAATT	ATAAGAAAGG	GT'TTGGAAAC	ATTGACGGAG	AATACTGGCT	1500
TGGACTGGAA	AATATCTATA	TGCTTAGCAA	TCAAGATAAT	TACAAGTTAT	1550
TGATTGAATT	AGAAGACTGG	AGTGATAAAA	AAGTCTATGC	AGAATACAGC	1600
AGCTTTCGTC	TGGAACCTGA	AAGTGAATTC	TATAGACTGC	GCCTGGGAAC	1650
TTACCAGGGA	AATGCAGGGG	ATTCTATGAT	GTGGCATAAT	GGTAAACAAT	1700
TCACCACACT	GGACAGAGAT	AAAGATATGT	ATGCAGGAAA	CTGCGCCAC	1750
TTTCATAAAG	GAGGCTGGTG	GTACAATGCC	TGTGCACATT	CTAACCTAAA	1800
TGGAGTATGG	TACAGAGGAG	GCCATTACAG	AAGCAAGCAC	CAAGATGGAA	1850
TTTTCTGGGC	CGAATACAGA	GGCGGGTCAT	ACTCCTTAAG	AGCAGTTCAG	1900
ATGATGATCA	AGCCTATTGA	CTGAAGAGAG	ACACTCGCCA	ATTTAAATGA	1950
CACAGAACTT	TGTACTTTTTC	AGCTCTTAAA	AATGTAAATG	TTACATGTAT	2000
ATTACTTGGC	ACAATTTTATT	TCTACACAGA	AAGTTTTTTAA	AATGAATTTT	2050
ACCGTAACTA	TAAAAGGGAA	CCTATAAATG	TAGTTTCATC	TGTCGTCAAT	2100
TACTGCAGAA	AATTATGTGT	ATCCACAACC	TAGTTATTTT	AAAAATTATG	2150
TTGACTAAAT	ACAAAGTTTG	TTTTCTAAAA	TGTAAATATT	TGCCACAATG	2200
TAAAGCAAAT	CTTAGCTATA	TTTTTAAATCA	TAAATAACAT	GTTCAAGATA	2250
CTTAACAATT	TATTTAAAAAT	CTAAGATTGC	TCTAACGTCT	AGTGAAAAAA	2300
ATATTTTTTTA	AATTTTCAGCC	AAATAATGCA	TTTTATTTTTA	TAAAAATACA	2350
GACAGAAAAT	TAGGGAGAAA	CTTC'TAGTTT	TGCCAATAGA	AAATGTTCTT	2400
CCATTGAATA	AAAGTTATTT	CAAATTGAAT	TTGTGCCTTT	CACACGTAAT	2450
GATTAAATCT	GAATTCTTAA	TAATATATCC	TATGCTGATT	TTCCCAAAC	2500
ATGACCCATA	GTATTAAATA	CATATCATTT	TTAAAAATAA	AAAAAACCC	2550
AAAAATAATG	CATGCATAAT	TTAAATGGTC	AATTTATAAA	GACAAATCTA	2600
TGAATGAATT	TTTCAGTGTT	ATCTTCATAT	GATATGCTGA	ACACCAAAT	2650
CTCCAGAAAT	GCATTTTATG	TAGTTC'TAAA	ATCAGCAAAA	TATTGGTATT	2700
ACAAAAATGC	AGAATATTTA	GTGTGCTACA	GATCTGAATT	ATAGTTCTAA	2750

TTTATTATTA CTTTTTTTCT AATTTACTGA TCTTACTACT ACAAAGAAAA 2800
 AAAAACCCTAA CCCATCTGCA ATTCAAATCA GAAAGTTTGG ACAGCTTTAC 2850
 AAGTATTAGT GCATGCTCAG AACAGGTGGG ACTAAAACAA ACTCAAGGAA 2900
 CTGTTGGCTG TTTTCCCGAT ACTGAGAATT CAACAGCTCC AGAGCAGAAG 2950
 CCACAGGGGC ATAGCTTAGT CCAAAGTGGT AATTTTCATTT TACAGTGTAT 3000
 GTAACGCTTA GTCTCACAGT GTCTTTAACT CATCTTTGCA ATCAACAAC 3050
 TTACTAGTGA CTTTCTGGAA CAATTTTCCTT TCAGGAATAC ATATTCACTG 3100
 CTTAGAGGTG ACCTTGCTT AATATATTTG TGAAGTTAAA ATTTTAAAGA 3150
 TAGCTCATGA AACTTTTGCT TAAGCAAAAA GAAAACCTCG AATTGAAATG 3200
 TGTGAGGCAA ACTATGCATG GGAATAGCTT AATGTGAAGA TAATCATTTG 3250
 GACAACTCAA ATCCATCAAC ATGACCAATG TTTTTCATCT GCCACATCTC 3300
 AAAATAAAAC TTCTGGTGAA ACAAATTAAA CAAAATATCC AAACCTCAAA 3350
 AAAAA 3355

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Lys	Thr	Phe	Thr	Trp	Thr	Leu	Gly	Val	Leu	Phe	Phe	Leu	Leu	1	5	10	15
Val	Asp	Thr	Gly	His	Cys	Arg	Gly	Gly	Gln	Phe	Lys	Ile	Lys	Lys	20	25	30	
Ile	Asn	Gln	Arg	Arg	Tyr	Pro	Arg	Ala	Thr	Asp	Gly	Lys	Glu	Glu	35	40	45	
Ala	Lys	Lys	Cys	Ala	Tyr	Thr	Phe	Leu	Val	Pro	Glu	Gln	Arg	Ile	50	55	60	
Thr	Gly	Pro	Ile	Cys	Val	Asn	Thr	Lys	Gly	Gln	Asp	Ala	Ser	Thr	65	70	75	
Ile	Lys	Asp	Met	Ile	Thr	Arg	Met	Asp	Leu	Glu	Asn	Leu	Lys	Asp	80	85	90	
Val	Leu	Ser	Arg	Gln	Lys	Arg	Glu	Ile	Asp	Val	Leu	Gln	Leu	Val	95	100	105	
Val	Asp	Val	Asp	Gly	Asn	Ile	Val	Asn	Glu	Val	Lys	Leu	Leu	Arg	110	115	120	
Lys	Glu	Ser	Arg	Asn	Met	Asn	Ser	Arg	Val	Thr	Gln	Leu	Tyr	Met	125	130	135	

Gln	Leu	Leu	His	Glu 140	Ile	Ile	Arg	Lys	Arg 145	Asp	Asn	Ser	Leu	Glu 150
Leu	Ser	Gln	Leu	Glu 155	Asn	Lys	Ile	Leu	Asn 160	Val	Thr	Thr	Glu	Met 165
Leu	Lys	Met	Ala	Thr 170	Arg	Tyr	Arg	Glu	Leu 175	Glu	Val	Lys	Tyr	Ala 180
Ser	Leu	Thr	Asp	Leu 185	Val	Asn	Asn	Gln	Ser 190	Val	Met	Ile	Thr	Leu 195
Leu	Glu	Glu	Gln	Cys 200	Leu	Arg	Ile	Phe	Ser 205	Arg	Gln	Asp	Thr	His 210
Val	Ser	Pro	Pro	Leu 215	Val	Gln	Val	Val	Pro 220	Gln	His	Ile	Pro	Asn 225
Ser	Gln	Gln	Tyr	Thr 230	Pro	Gly	Leu	Leu	Gly 235	Gly	Asn	Glu	Ile	Gln 240
Arg	Asp	Pro	Gly	Tyr 245	Pro	Arg	Asp	Leu	Met 250	Pro	Pro	Pro	Asp	Leu 255
Ala	Thr	Ser	Pro	Thr 260	Lys	Ser	Pro	Phe	Lys 265	Ile	Pro	Pro	Val	Thr 270
Phe	Ile	Asn	Glu	Gly 275	Pro	Phe	Lys	Asp	Cys 280	Gln	Gln	Ala	Lys	Glu 285
Ala	Gly	His	Ser	Val 290	Ser	Gly	Ile	Tyr	Met 295	Ile	Lys	Pro	Glu	Asn 300
Ser	Asn	Gly	Pro	Met 305	Gln	Leu	Trp	Cys	Glu 310	Asn	Ser	Leu	Asp	Pro 315
Gly	Gly	Trp	Thr	Val 320	Ile	Gln	Lys	Arg	Thr 325	Asp	Gly	Ser	Val	Asn 330
Phe	Phe	Arg	Asn	Trp 335	Glu	Asn	Tyr	Lys	Lys 340	Gly	Phe	Gly	Asn	Ile 345
Asp	Gly	Glu	Tyr	Trp 350	Leu	Gly	Leu	Glu	Asn 355	Ile	Tyr	Met	Leu	Ser 360
Asn	Gln	Asp	Asn	Tyr 365	Lys	Leu	Leu	Ile	Glu 370	Leu	Glu	Asp	Trp	Ser 375
Asp	Lys	Lys	Val	Tyr 380	Ala	Glu	Tyr	Ser	Ser 385	Phe	Arg	Leu	Glu	Pro 390
Glu	Ser	Glu	Phe	Tyr 395	Arg	Leu	Arg	Leu	Gly 400	Thr	Tyr	Gln	Gly	Asn 405
Ala	Gly	Asp	Ser	Met 410	Met	Trp	His	Asn	Gly 415	Lys	Gln	Phe	Thr	Thr 420
Leu	Asp	Arg	Asp	Lys 425	Asp	Met	Tyr	Ala	Gly 430	Asn	Cys	Ala	His	Phe 435
His	Lys	Gly	Gly	Trp	Trp	Tyr	Asn	Ala	Cys	Ala	His	Ser	Asn	Leu

Table 1. Mean values of the variables measured during the 60-min test

				440						445					450
Asn	Gly	Val	Trp	Tyr	Arg	Gly	Gly	His	Tyr	Arg	Ser	Lys	His	Gln	
				455					460					465	
Asp	Gly	Ile	Phe	Trp	Ala	Glu	Tyr	Arg	Gly	Gly	Ser	Tyr	Ser	Leu	
				470					475					480	
Arg	Ala	Val	Gln	Met	Met	Ile	Lys	Pro	Ile	Asp					
				485					490	491					

(2) INFORMATION FOR SEQ ID NO:5:

- (A) LENGTH: 1780 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

GGCTCAGAGG	CCCCACTGGA	CCCTCGGCTC	TTCTTTGGAC	TTCTTGTGTG	50
TTCTGTGAGC	TTCGCTGGAT	TCAGGGTCTT	GGGCATCAGA	GGTGAGAGGG	100
TGGGAAGGTC	CGCCGCGATG	GGGAAGCCCT	GGCTGCGTGC	GCTACAGCTG	150
CTGCTCCTGC	TGGGCGCGTC	GTGGGCGCGG	GCGGGCGCCC	CGCGCTGCAC	200
CTACACCTTC	GTGCTGCCCC	CGCAGAAGTT	CACGGGCGCT	GTGTGCTGGA	250
GCGGCCCCGC	ATCCACGCGG	GCGACGCCCC	AGGCCGCCAA	CGCCAGCGAG	300
CTGGCGGCGC	TGCGCATGCG	CGTCGGCCGC	CACGAGGAGC	TGTTACGCGA	350
GCTGCAGAGG	CTGGCGGCGG	CCGACGGCGC	CGTGGCCGGC	GAGGTGCGCG	400
CGCTGCGCAA	GGAGAGCCGC	GGCCTGAGCG	CGCGCCTGGG	CCAGTTGCGC	450
GCGCAGCTGC	AGCACGAGGC	GGGGCCCCGG	GCGGGCCCCG	GGGCGGATCT	500
GGGGGCGGAG	CCTGCCGCGG	CGCTGGCGCT	GCTCGGGGAG	CGCGTGCTCA	550
ACGCGTCCGC	CGAGGCTCAG	CGCGCAGCCG	CCCGGTTCCA	CCAGCTGGAC	600
GTCAAGTTCC	GCGAGCTGGC	GCAGCTCGTC	ACCCAGCAGA	GCAGTCTCAT	650
CGCCCGCCTG	GAGCGCCTGT	GCCCGGGAGG	CGCGGGCGGG	CAGCAGCAGG	700
TCCTGCCGCC	ACCCCCACTG	GTGCCCTGTGG	TTCCGGTCCG	TCTTGTGGGT	750
AGCACCAGTG	ACACCAGTAG	GATGCTGGAC	CCAGCCCCAG	AGCCCCAGAG	800
AGACCAGACC	CAGAGACAGC	AGGAGCCCAT	GGCTTCTCCC	ATGCCTGCAG	850
GTCACCCTGC	GGTCCCCACC	AAGCCTGTGG	GCCCGTGGCA	GGATTGTGCA	900
GAGGCCCGCC	AGGCAGGCCA	TGAACAGAGT	GGAGTGTATG	AACTGCGAGT	950
GGGCCGTCAC	GTAGTGTCAG	TATGGTGTGA	GCAGCAACTG	GAGGGTGGAG	1000

GCTGGACTGT	GATCCAGCGG	AGGCAAGATG	GTTCAGTCAA	CTTCTTCACT	1050
ACCTGGCAGC	ACTATAAGGC	GGGCTTTGGG	CGGCCAGACG	GAGAATACTG	1100
GCTGGGCCTT	GAACCCGTGT	ATCAGCTGAC	CAGCCGTGGG	GACCATGAGC	1150
TGCTGGTTCT	CCTGGAGGAC	TGGGGGGGCC	GTGGAGCACG	TGCCCACTAT	1200
GATGGCTTCT	CCCTGGAACC	CGAGAGCGAC	CACTACCGCC	TGCGGCTTGG	1250
CCAGTACCAT	GGTGATGCTG	GAGACTCTCT	TTCCTGGCAC	AATGACAAGC	1300
CCTTCAGCAC	CGTGGATAGG	GACCGAGACT	CCTATTCTGG	TAACTGTGCC	1350
CTGTACCAGC	GGGGAGGCTG	GTGGTACCAT	GCCTGTGCCC	ACTCCAACCT	1400
CAACGGTGTG	TGGCACACAG	GCGGCCACTA	CCGAAGCCGC	TACCAGGATG	1450
GTGTCTACTG	GGCTGAGTTT	CGTGGTGGGG	CATATTCTCT	CAGGAAGGCC	1500
GCCATGCTCA	TTCGGCCCCC	GAAGCTGTGA	CTCTGTGTTC	CTCTGTCCCC	1550
TAGGCCCTAG	AGGACATTGG	TCAGCAGGAG	CCCAAGTTGT	TC'TGGCCACA	1600
CCTTCTTTGT	GGCTCAGTGC	CAATGTGTCC	CACAGAACTT	CCCCTGTGG	1650
ATCTGTGACC	CTGGGCGCTG	AAAATGGGAC	CCAGGAATCC	CCCCCGTCAA	1700
TATCTTGGCC	TCAGATGGCT	CCCCAAGGTC	ATTCATATCT	CGGTTTGAGC	1750
TCATATCTTA	TAATAACACA	AAGTAGCCAC	1780		

(2) INFORMATION FOR SEO ID NO:6:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

[illegible]

(2) INFORMATION FOR SEO ID NO:7:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

(2) INFORMATION FOR SEQ ID NO:8:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

(2) INFORMATION FOR SEQ ID NO:9:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

(2) INFORMATION FOR SEQ ID NO:10:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CAGGTTATCC CAGAGATTTA ATGCCACCA 29

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TTGGTGGGAG AAGTTGCCAG ATCAGGTGGT GGCA 34

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTCACACCAT AACTGCATTG GTCCA 25

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACGTAGTTCC AGTATGGTGT GAGCAGCAAC TGGA 34

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AGTCCAGCCT CCACCCTCCA GTTGCT 26

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs

(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCCCAGTCCT CCAGGAGAAC CAGCA 25

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2042 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCGGACGCGT GGGTGAAATT GAAAATCAAG ATAAAAATGT TCACAATTAA 50
GCTCCTTCTT TTTATTGTTC CTCTAGTTAT TTCCTCCAGA ATTGATCAAG 100
ACAATTCATC ATTTGATTCT CTATCTCCAG AGCCAAAATC AAGATTGCT 150
ATGTTAGACG ATGTAAAAAT TTTAGCCAAT GGCCTCCTTC AGTTGGGACA 200
TGGTCTTAAA GACTTTGTCC ATAAGACGAA GGGCCAAATT AATGACATAT 250
TTCAAAAACCT CAACATATTT GATCAGTCTT TTTATGATCT ATCGCTGCAA 300
ACCAGTGAAA TCAAAGAAGA AGAAAAGGAA CTGAGAAGAA CTACATATAA 350
ACTACAAGTC AAAAATGAAG AGGTAAAGAA TATGTCACTT GAACTCAACT 400
CAAAACTTGA AAGCCTCCTA GAAGAAAAAA TTCTACTTCA ACAAAAAGTG 450
AAATATTTAG AAGAGCAACT AACTAACTTA ATTCAAAATC AACCTGAAAC 500
TCCAGAACAC CCAGAAGTAA CTTCACTTAA AACTTTTGTA GAAAAACAAG 550
ATAATAGCAT CAAAGACCTT CTCCAGACCG TGGAAGACCA ATATAAACAA 600
TTAAACCAAC AGCATAGTCA AATAAAAGAA ATAGAAAATC AGCTCAGAAG 650
GACTAGTATT CAAGAACCCA CAGAAATTTT TCTATCTTCC AAGCCAAGAG 700
CACCAAGAAC TACTCCCTTT CTTCAAGTTGA ATGAAATAAG AAATGTAAAA 750
CATGATGGCA TTCCTGCTGA ATGTACCACC ATTTATAACA GAGGTGAACA 800
TACAAGTGGC ATGTATGCCA TCAGACCCAG CAACTCTCAA GTTTTTTCATG 850
TCTACTGTGA TGTTATATCA GGTAGTCCAT GGACATTAAT TCAACATCGA 900
ATAGATGGAT CACAAAACCT CAATGAAACG TGGGAGAACT ACAAATATGG 950
TTTTGGGAGG CTTGATGGAG AATTTTGGTT GGGCCTAGAG AAGATATACT 1000
CCATAGTGAA GCAATCTAAT TATGTTTTAC GAATTGAGTT GGAAGACTGG 1050

AAAGACAACA	AACATTATAT	TGAATATTCT	TTTTACTTGG	GAAATCACGA	1100
AACCAACTAT	ACGCTACATC	TAGTTGCGAT	TACTGGCAAT	GTCCCCAATG	1150
CAATCCCGGA	AAACAAAGAT	TTGGTGTTTT	CTACTTGGGA	TCACAAAGCA	1200
AAAGGACACT	TCAACTGTCC	AGAGGGTTAT	TCAGGAGGCT	GGTGGTGGCA	1250
TGATGAGTGT	GGAGAAAACA	ACCTAAATGG	TAAATATAAC	AAACCAAGAG	1300
CAAAATCTAA	GCCAGAGAGG	AGAAGAGGAT	TATCTTGGAA	GTCTCAAAAT	1350
GGAAGGTTAT	ACTCTATAAA	ATCAACCAAA	ATGTTGATCC	ATCCAACAGA	1400
TTCAGAAAGC	TTTGAATGAA	CTGAGGCAAT	TTAAAGGCAT	ATTTAACCAT	1450
TAACTCATTC	CAAGTTAATG	TGGTCTAATA	ATCTGGTATA	AATCCTTAAG	1500
AGAAAGCTTG	AGAAATAGAT	TTTTTTTTATC	TTAAAGTCAC	TGTCCTATTTA	1550
AGATTAAACA	TACAATCACA	TAACCTTAAA	GAATACCGTT	TACATTTCTC	1600
AATCAAAATT	CTTATAATAC	TATTTGTTTT	AAATTTTGTG	ATGTGGGAAT	1650
CAATTTTAGA	TGGTCACAAT	CTAGATTATA	ATCAATAGGT	GAACTTATTA	1700
AATAACTTTT	CTAAATAAAA	AATTTAGAGA	CTTTTATTTT	AAAAGGCATC	1750
ATATGAGCTA	ATATCACAAC	TTTCCCAGTT	TAAAAAATA	GTACTCTTGT	1800
TAAAC'TCTA	AAC'TTGACTA	AATACAGAGG	ACTGGTAATT	GTACAGTTCT	1850
TAAATGTTGT	AGTATTAAAT	TCAAAACTAA	AAATCGTCAG	CACAGAGTAT	1900
GTGTAAAAAT	CTGTAATACA	AATTTT'TAAA	CTGATGC'TTC	ATTTTGTCTAC	1950
AAAATAATTT	GGAGTAAATG	TTTGATATGA	TTTATTTTATG	AAACCTAATG	2000
AAGCAGAATT	AAATACTGTA	TTAAAAATAAG	TTTCGCTGTCT	TT	2042

(2) INFORMATION FOR SEQ ID NO:17:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

